AMENDMENTS TO THE SPECIFICATION

Please amend the specification as follows:

Paragraph 14 (page 5):

Figure 1. Alignments of tick-borne encephalitis virus E, hepatitis C virus E1 and classical swine fever virus E2 glycoproteins. Panel A: ~~Amino acids are numbered from the beginning~~ Certain portions of the TBEV E (SEQ ID NO:66), HCV E1 (SEQ ID NO:67), [[and]] CSFV E2 (SEQ ID NO:68) and HCV E2 (SEQ ID NO:71) polyproteins are aligned. ~~in this and subsequent figures.~~ Bracketed HCV insert sequences (HCV E1, SEQ ID NO:69; HCV E2, SEQ ID NO:70) are wrapped and do not represent an alignment comparison (Fig. 1A cont.). "(:)" refers to identical amino acids. "(.)" refers to chemically similar amino acids. Panel B: Linear arrangement of the domain structure of TBEV E as determined by Rey et al. (1995). Regions of significant sequence similarities to TBEV E in HCV E1 and E2 and CSFV E2 as determined by the PRSS3 sequence alignment program are indicated. Probabilities (p-values) are based on 1000 shuffles.

Paragraph 16 (page 5):

Figure 3. ~~Alignments of the precursor of tick borne encephalitis virus small membrane protein, prM, and classical swine fever virus E1.~~ Panel A: Aligned portions of the TBEV small membrane protein (prM, SEQ ID NO:72) and CSFV E1 (SEQ ID NO:73) protein. ~~Alignments~~ alignments were constructed as detailed in the text. Panel B: Linear arrangement of TBEV prM and CSFV E1 with a region of sequence similarity determined by the PPSS3 algorithm indicted.

Paragraph 18 (bridging pages 5 and 6):

Figure 5. Comparison of human immunodeficiency virus transmembrane glycoprotein (TM) with hepatitis C virus envelope glycoprotein 1 (E1). ~~Panel A:~~ Presented on the left side of the figure is an updated structure of HIV-1 TM sequence (SEQ ID NO:74) from Gallaher et al. (1989) with structural motifs indicated in rainbow order. Amino acids are numbered from the beginning of the Env polyprotein. HIV-1 TM is truncated after the transmembrane domain. The precise ends of the TM N- and C-helices are unclear because of conflicting structural data. No attempt was made to align the N- and C-helices, although points of contact are solved in the coiled-coil formations. Positions of known neutralizing epitopes on TM are indicated, as well as sequences corresponding to peptides CS3 and DP178 (T20) (Qureshi et al., 1990; Wild et al., 1994) that inhibit HIV-1 infectivity. ~~Panel B:~~ Presented on the right side of the figure is the structure ~~Structure~~ of HCV E1 sequence (SEQ ID NO:75) with motifs that are shared with HIV-1 TM. Boxed arrows are predicted beta sheet structures that are similar to the indicated β sheets of TBEV E. Predicted α helical structures are outlined. Arrows denote directions that the HCV E1 structure could fold in three dimensions.

Sequence Listing:

Please replace the Sequence Listing filed with the Preliminary Amendment and Priority Notice on April 22, 2005 with the amended Sequence Listing (forty pages total) filed herewith.